



crt sequences.ST25  
SEQUENCE LISTING

<110> St. Boniface General Hospital Research Centre  
Mesaeli, Nasrin  
<120> Transgenic Mouse over-expressing calreticulin (CRT) in vascular  
smooth muscle cells  
<130> 81190-2602  
<150> US 60/455399  
<151> 2003-03-18  
<160> 24  
<170> PatentIn version 3.2  
<210> 1  
<211> 2655  
<212> DNA  
<213> Artificial  
<220>  
<223> artificial construct of sm22a promoter and CRT cDNA  
  
<220>  
<221> CDS  
<222> (1319)..(2653)  
<223> CRT coding sequence

<400> 1  
ccccttcctt cagatgccac aaggagggtgc tggagttcta tgcaccaata gcttaaacca 60  
gccaggctgg ctgttagtgg a ttgagcgtct gaggctgcac ctctctggcc tgcagccagt 120  
tcctgggtga gactgaccct gcctgagggt tctctccctc cctctctcta ctcctttcct 180  
ccctctccct ctccctctct ctgtttcctg aggtttccag gattggggat gggactcaga 240  
gacaccacta aagccttacc ttttaagaag ttgcattcag tgagtgtgt agacatagca 300  
cagatagggg cagaggagag ctggttctgt ctccactgtg ttttgtcttg ggtactgaac 360  
tcagaccatc aggtgtgata gcagttgtct ttaaccctaa ccctgagcct gtctcacctg 420  
tcccttccca agaccactga agctaggtgc aagataagt gggacccttt ctgaggtgg 480  
aggatctttc acgataagga ctatttgaa gggagggagg gtgacactgt cctagtcctc 540  
ttaccctagt gtcctccagc cttgccaggc cttaaacatc cgcccattgt caccgctcta 600  
gaaggggcca gggttgactt gctgctaaac aaggcactcc ctagagaagc acccgctaga 660  
agcataaccat acctgtggc aggatgaccc atgttctgcc acgcacttgg tagccttgaa 720  
aaggccactt tgaacctcaa ttttctcaac tgttaaatgg ggtggtaact gctatctcat 780  
aataaagggg aacgtgaaag gaaggcgaaa gcatagtgcc tgggtgtgca gccaggctgc 840  
agtcaagact agttcccacc aactcgattt taaagccttg caagaagggtg gcttgggtgt 900  
cccttgcagg ttcctttgtc gggccaaact ctagaatgcc tcccccttcc tttctcattg 960

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aagagcagac ccaagtccgg gtaacaagga agggtttcag ggtcctgccc ataaaaggtt	1020
tttcccggcc gccctcagca ccgccccgcc ccgacccccc cagcatctcc aaagcatgca	1080
gagaatgtct ccggctgccc ccgacagact gctccaacctt ggtgtcttcc cccaaatatg	1140
gagcctgtgt ggagttagtg gggcgccccg gggtggtgag ccaagcagac ttccatggc	1200
agggaggggc gccagcggac ggcagagggg tgacatcaact gccttaggcgg cctttaaacc	1260
cctcacccag ccggcgcccc accgagctcg gatccactag tccagtgtgg tggattc	1318
atg ctg ctc cct gtg ccg ctg ctc ggc ctg ctc ggc ctg gcc gcc Met Leu Leu Pro Val Pro Leu Leu Gly Leu Leu Gly Leu Ala Ala	1366
1 5 10 15	
gcc gag ccc gtc gtc tac ttc aag gag cag ttt ctg gac gga gat ggg Ala Glu Pro Val Val Tyr Phe Lys Glu Gln Phe Leu Asp Gly Asp Gly	1414
20 25 30	
tgg acc gag cgc tgg atc gaa tcc aaa cac aag tcc gat ttt ggc aaa Trp Thr Glu Arg Trp Ile Glu Ser Lys His Lys Ser Asp Phe Gly Lys	1462
35 40 45	
ttc gtc ctc agt tcg ggc aag ttc tac ggc gat cag gag aaa gat aaa Phe Val Leu Ser Ser Gly Lys Phe Tyr Gly Asp Gln Glu Lys Asp Lys	1510
50 55 60	
ggg ctg cag acc agc cag gac gcc cgc ttc tac gcc ctg tcg gcc cga Gly Leu Gln Thr Ser Gln Asp Ala Arg Phe Tyr Ala Leu Ser Ala Arg	1558
65 70 75 80	
ttc gag ccg ttc agc aac aag ggc cag cca ctg gtg gtg cag cca gcc Phe Glu Pro Phe Ser Asn Lys Gly Gln Pro Leu Val Val Gln Pro Ala	1606
85 90 95	
agg acg ccc gct tct acg ccc tgt cgg ccc gat tcg agc cgt tca gca Arg Thr Pro Ala Ser Thr Pro Cys Arg Pro Asp Ser Ser Arg Ser Ala	1654
100 105 110	
aca agg gcc agc cac tgg tgg tgc agt tca ccg tga aac acg acg aga Thr Arg Ala Ser His Trp Trp Cys Ser Ser Pro Asn Thr Ser Arg	1702
115 120 125	
aca ttg act gcg ggg gcg gct acg tga agc tgt ttc cgg ccg gcc tgg Thr Leu Thr Ala Gly Ala Ala Thr Ser Cys Phe Arg Pro Ala Trp	1750
130 135 140	
acc aga agg aca tgc acg ggg act ctg agt aca aca tca tgt ttg gtc Thr Arg Arg Thr Cys Thr Gly Thr Leu Ser Thr Thr Ser Cys Leu Val	1798
145 150 155	
ctg aca tct gtg gcc ccg gca cca aga agg ttc acg tca tct tca act Leu Thr Ser Val Ala Pro Ala Pro Arg Arg Phe Thr Ser Ser Ser Thr	1846
160 165 170	
aca agg gca aga acg tgc tga tca aca agg aca tcc gtt gca agg acg Thr Arg Ala Arg Thr Cys Ser Thr Arg Thr Ser Val Ala Arg Thr	1894
175 180 185	
acg agt tca cac acc tgt aca cgc tga tcg tgc ggc cgg aca aca cgt Thr Ser Ser His Thr Cys Thr Arg Ser Cys Gly Arg Thr Thr Arg	1942

## crt sequences.ST25

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<210> 2  
<211> 123  
<212> PRT  
<213> Artificial

<220>  
<223> Synthetic Construct

<400> 2

Met Leu Leu Pro Val Pro Leu Leu Leu Gly Leu Leu Gly Leu Ala Ala  
1 5 10 15

Ala Glu Pro Val Val Tyr Phe Lys Glu Gln Phe Leu Asp Gly Asp Gly  
20 25 30

Trp Thr Glu Arg Trp Ile Glu Ser Lys His Lys Ser Asp Phe Gly Lys  
35 40 45

Phe Val Leu Ser Ser Gly Lys Phe Tyr Gly Asp Gln Glu Lys Asp Lys  
50 55 60

Gly Leu Gln Thr Ser Gln Asp Ala Arg Phe Tyr Ala Leu Ser Ala Arg  
65 70 75 80

Phe Glu Pro Phe Ser Asn Lys Gly Gln Pro Leu Val Val Gln Pro Ala  
85 90 95

Arg Thr Pro Ala Ser Thr Pro Cys Arg Pro Asp Ser Ser Arg Ser Ala  
100 105 110

Thr Arg Ala Ser His Trp Trp Cys Ser Ser Pro  
115 120

<210> 3  
<211> 12  
<212> PRT  
<213> Artificial

<220>  
<223> Synthetic Construct

<400> 3

Asn Thr Ser Arg Thr Leu Thr Ala Gly Ala Ala Thr  
1 5 10

<210> 4  
<211> 45  
<212> PRT  
<213> Artificial

<220>  
<223> Synthetic Construct

crt sequences.ST25

<400> 4

Ser Cys Phe Arg Pro Ala Trp Thr Arg Arg Thr Cys Thr Gly Thr Leu  
1 5 10 15

Ser Thr Thr Ser Cys Leu Val Leu Thr Ser Val Ala Pro Ala Pro Arg  
20 25 30

Arg Phe Thr Ser Ser Thr Thr Arg Ala Arg Thr Cys  
35 40 45

<210> 5

<211> 17

<212> PRT

<213> Artificial

<220>

<223> Synthetic Construct

<400> 5

Ser Thr Arg Thr Ser Val Ala Arg Thr Thr Ser Ser His Thr Cys Thr  
1 5 10 15

Arg

<210> 6

<211> 9

<212> PRT

<213> Artificial

<220>

<223> Synthetic Construct

<400> 6

Ser Cys Gly Arg Thr Thr Arg Met Arg  
1 5

<210> 7

<211> 23

<212> PRT

<213> Artificial

<220>

<223> Synthetic Construct

<400> 7

Arg Leu Thr Thr Ala Arg Trp Ser Arg Ala Pro Trp Arg Met Thr Gly  
1 5 10 15

Thr Ser Tyr Pro Pro Arg Arg

20

crt sequences.ST25

<210> 8  
<211> 56  
<212> PRT  
<213> Artificial

<220>  
<223> Synthetic Construct

<400> 8

Arg Thr Gln Met Pro Arg Ser Leu Lys Thr Gly Thr Ser Gly Pro Arg  
1 5 10 15

Ser Thr Thr Pro Arg Thr Pro Ser Pro Arg Thr Gly Thr Ser Pro Ser  
20 25 30

Thr Ser Pro Thr Arg Thr Arg Arg Ser Pro Lys Thr Gly Thr Lys Lys  
35 40 45

Trp Thr Glu Ser Gly Ser Arg Arg  
50 55

<210> 9  
<211> 91  
<212> PRT  
<213> Artificial

<220>  
<223> Synthetic Construct

<400> 9

Phe Arg Thr Pro Ser Thr Arg Val Ser Gly Ser Arg Gly Arg Ser Thr  
1 5 10 15

Thr Pro Ile Thr Lys Ala Pro Gly Ser Thr Pro Lys Ser Thr Thr Pro  
20 25 30

Ser Thr Arg Pro Thr Leu Thr Ser Met Pro Thr Thr Ala Leu Pro Cys  
35 40 45

Trp Ala Trp Thr Ser Gly Arg Ser Ser Arg Ala Pro Ser Ser Thr Thr  
50 55 60

Ser Ser Ser Pro Thr Met Arg Arg Thr Gln Arg Ser Leu Ala Thr Arg  
65 70 75 80

Arg Gly Ala Ser Pro Arg Arg Pro Arg Ser Arg  
85 90

<210> 10

crt sequences.ST25

<211> 9  
<212> PRT  
<213> Artificial

<220>  
<223> Synthetic Construct

<400> 10

Lys Thr Ser Arg Thr Arg Ser Ser Gly  
1 5

<210> 11  
<211> 51  
<212> PRT  
<213> Artificial

<220>  
<223> Synthetic Construct

<400> 11

Arg Arg Arg Arg Arg Arg Ser Gly Arg Arg Arg Arg Arg Pro Arg  
1 5 10 15

Arg Thr Arg Arg Thr Arg Thr Thr Arg Arg Thr Arg Met Arg Thr Arg  
20 25 30

Arg Thr Arg Thr Arg Arg Arg Arg Arg Arg Pro Pro Ala Arg Pro Arg  
35 40 45

Thr Ser Cys  
50

<210> 12  
<211> 2691  
<212> DNA  
<213> Artificial

<220>  
<223> construct of SM22a promoter and CRT cDNA with HA tag inserted  
into CRT cDNA

<220>  
<221> CDS  
<222> (1319)..(2689)

<220>  
<221> misc\_feature  
<222> (2635)..(2670)  
<223> HA insertion

<400> 12  
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gccaggctgg ctgttagtgga ttgagcgtct gaggctgcac ctctctggcc tgcagccagt 120

crt sequences.ST25		
tcctgggtga	gactgaccct	180
gcctgagggt	tctctccctc	
ccctctccct	cctctctcta	
ctccctctct	ctccttcctg	240
ctgtttcctg	aggtttccag	
gattggggat	gggactcaga	
gacaccacta	aagccttacc	300
tttaagaag	ttgcatttag	
tgagtgtgt	agacatagca	
cagatagggg	cagaggagag	360
ctgggtctgt	ctccactgtg	
tttggcttg	ggtactgaac	
tcagaccatc	aggtgtgata	420
gcagttgtct	ttaaccctaa	
ccctgagcct	gtctcacctg	
tccctccca	agaccactga	480
agcttaggtgc	aagataagtg	
gggacccttt	ctgaggttgt	
aggatcttc	acgataagga	540
ctatttgaa	gggagggagg	
gtgacactgt	cctagtcctc	
ttaccctagt	gtcctccagc	600
cttgcaggc	cttaaacatc	
cgcccattgt	caccgctcta	
gaaggggcca	ggggttgactt	660
gctgctaaac	aaggcactcc	
ctagagaagc	acccgctaga	
agcataccat	acctgtggc	720
aggatgaccc	atgttctgcc	
acgcacttgg	tagccttgga	
aaggccactt	tgaacctcaa	780
ttttctcaac	tgttaaatgg	
ggtggttaact	gctatctcat	
aataaagggg	aacgtgaaag	840
gaaggcgaaa	gcatagtgcc	
tggttgtgca	gccaggctgc	
agtcaagact	agttcccacc	900
aactcgattt	taaagccttg	
caagaagggtg	gcttgggtgt	
cccttgcagg	ttcctttgtc	960
gggccaaact	ctagaatgcc	
tcccccttcc	tttctcattg	
aagagcagac	ccaagtccgg	1020
gtaacaagga	agggtttcag	
ggtcctgccc	ataaaaaggtt	
tttcccgccc	gccctcagca	1080
ccgccccgccc	ccgacccccc	
cagcatctcc	aaagcatgca	
gagaatgtct	ccggctgccc	1140
ccgacagact	gctccaactt	
ggtgtctttc	cccaaataatg	
gagcctgtgt	ggagtgagtg	1200
gggcggcccc	gggtggtgag	
ccaagcagac	ttccatgggc	
agggaggggc	gccagcggac	1260
ggcagagggg	tgacatcaact	
gcctaggcgg	cctttaaacc	
cctcacccag	ccggcgcccc	1318
accgagctcg	gatccactag	
tccagtgtgg	ttggaaattc	
atg ctg ctc cct gtg ccg ctg ctc ggc ctg ctc ggc ctg gcc		1366
Met Leu Leu Pro Val Pro Leu Leu Leu Gly Leu Leu Gly Leu Ala Ala		
1 5 10 15		
gcc gag ccc gtc gtc tac ttc aag gag cag ttt ctg gac gga gat ggg		1414
Ala Glu Pro Val Val Tyr Phe Lys Glu Gln Phe Leu Asp Gly Asp Gly		
20 25 30		
tgg acc gag cgc tgg atc gaa tcc aaa cac aag tcc gat ttt ggc aaa		1462
Trp Thr Glu Arg Trp Ile Glu Ser Lys His Lys Ser Asp Phe Gly Lys		
35 40 45		
ttc gtc ctc agt tcg ggc aag ttc tac ggc gat cag gag aaa gat aaa		1510
Phe Val Leu Ser Ser Gly Lys Phe Tyr Gly Asp Gln Glu Lys Asp Lys		
50 55 60		
ggg ctg cag acc agc cag gac gcc cgc ttc tac gcc ctg tcg gcc cga		1558
Gly Leu Gln Thr Ser Gln Asp Ala Arg Phe Tyr Ala Leu Ser Ala Arg		
65 70 75 80		
ttc gag ccg ttc agc aac aag ggc cag cca ctg gtg gtg cag cca gcc		1606
Phe Glu Pro Phe Ser Asn Lys Gly Gln Pro Leu Val Val Gln Pro Ala		
85 90 95		

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agg acg ccc gct tct acg ccc tgt cggt ccc gat tcg agc cgt tca gca Arg Thr Pro Ala Ser Thr Pro Cys Arg Pro Asp Ser Ser Arg Ser Ala 100 105 110	1654
aca agg gcc agc cac tgg tgg tgc agt tca ccg tga aac acg agc aga Thr Arg Ala Ser His Trp Trp Cys Ser Ser Pro Asn Thr Ser Arg 115 120 125	1702
aca ttg act gcg ggg gcg gct acg tga agc tgt ttc ccg ccg gcc tgg Thr Leu Thr Ala Gly Ala Ala Thr Ser Cys Phe Arg Pro Ala Trp 130 135 140	1750
acc aga agg aca tgc acg ggg act ctg agt aca aca tca tgt ttg gtc Thr Arg Arg Thr Cys Thr Gly Thr Leu Ser Thr Thr Ser Cys Leu Val 145 150 155	1798
ctg aca tct gtg gcc ccg gca cca aga agg ttc acg tca tct tca act Leu Thr Ser Val Ala Pro Ala Pro Arg Arg Phe Thr Ser Ser Ser Thr 160 165 170	1846
aca agg gca aga acg tgc tga tca aca agg aca tcc gtt gca agg acg Thr Arg Ala Arg Thr Cys Ser Thr Arg Thr Ser Val Ala Arg Thr 175 180 185	1894
acg agt tca cac acc tgt aca cgc tga tcg tgc ggc ccg aca aca cgt Thr Ser Ser His Thr Cys Thr Arg Ser Cys Gly Arg Thr Thr Arg 190 195 200	1942
atg agg tga aga ttg aca aca gcc agg tgg agt cgg gct ccc tgg agg Met Arg Arg Leu Thr Thr Ala Arg Trp Ser Arg Ala Pro Trp Arg 205 210 215	1990
atg act ggg act tcc tac ccc cca aga aga taa agg acc cag atg cct Met Thr Gly Thr Ser Tyr Pro Pro Arg Arg Arg Thr Gln Met Pro 220 225 230	2038
cga agc ctg aag act ggg acg agc ggg cca aga tcg acg acc cca ccg Arg Ser Leu Lys Thr Gly Thr Ser Gly Pro Arg Ser Thr Thr Pro Arg 235 240 245 250	2086
act cca agc ccg agg act ggg aca agc ccg agc aca tcc ccg acc ccg Thr Pro Ser Pro Arg Thr Gly Thr Ser Pro Ser Thr Ser Pro Thr Arg 255 260 265	2134
acg cga aga agc ccg aag act ggg acg aag aaa tgg acg gag agt ggg Thr Arg Arg Ser Pro Lys Thr Gly Thr Lys Lys Trp Thr Glu Ser Gly 270 275 280	2182
agc cgc ccg tga ttc aga acc ccg agt aca agg gtg agt gga agc cgc Ser Arg Arg Phe Arg Thr Pro Ser Thr Arg Val Ser Gly Ser Arg 285 290 295	2230
ggc aga tcg aca acc ccg att aca aag gca cct gga tcc acc ccg aaa Gly Arg Ser Thr Thr Pro Ile Thr Lys Ala Pro Gly Ser Thr Pro Lys 300 305 310	2278
tcg aca acc ccg agt act cgc ccg acg cta aca tct atg cct acg aca Ser Thr Thr Pro Ser Thr Arg Pro Thr Leu Thr Ser Met Pro Thr Thr 315 320 325	2326
gct ttg ccg tgc tgg gct tgg acc tct ggc agg tca agt cgg gca cca Ala Leu Pro Cys Trp Ala Trp Thr Ser Gly Arg Ser Ser Arg Ala Pro	2374

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330	335	340	345	
tct tcg aca act tcc tca tca cca acg atg agg cgt acg cag agg agt Ser Ser Thr Thr Ser Ser Ser Pro Thr Met Arg Arg Thr Gln Arg Ser 350	355	360		2422
ttg gca acg aga cgt ggg gcg tca cca aga cgg ccg aga agc aga tga Leu Ala Thr Arg Arg Gly Ala Ser Pro Arg Arg Pro Arg Ser Arg 365	370	375		2470
aag aca agc agg acg agg agc agc gga tga agg agg agg agg agg aga Lys Thr Ser Arg Thr Arg Ser Ser Gly Arg Arg Arg Arg Arg Arg Arg 380	385		390	2518
aga agc gga agg agg agg agg agg ccg agg agg acg agg aca agg acg agg Arg Ser Gly Arg Arg Arg Arg Pro Arg Arg Thr Arg Arg Arg Thr Arg 395	400		405	2566
acg aca agg agg acg agg atg agg acg agg agg aca agg acg agg agg Thr Thr Arg Arg Thr Arg Met Arg Thr Arg Arg Thr Arg Thr Arg Arg 410	415		420	2614
agg agg agg cgg ccg ccg gcc tcg agt acc cat atg atg ttc ctg act Arg Arg Arg Pro Pro Ala Ser Ser Thr His Met Met Phe Leu Thr 425	430		435	2662
atg cta gac agg cca agg acg agc tgt ag Met Leu Asp Arg Pro Arg Thr Ser Cys 440	445			2691

<210> 13  
<211> 123  
<212> PRT  
<213> Artificial

<220>  
<223> Synthetic Construct

<400> 13

Met Leu Leu Pro Val Pro Leu Leu Leu Gly Leu Leu Gly Leu Ala Ala  
1 5 10 15

Ala Glu Pro Val Val Tyr Phe Lys Glu Gln Phe Leu Asp Gly Asp Gly  
20 25 30

Trp Thr Glu Arg Trp Ile Glu Ser Lys His Lys Ser Asp Phe Gly Lys  
35 40 45

Phe Val Leu Ser Ser Gly Lys Phe Tyr Gly Asp Gln Glu Lys Asp Lys  
50 55 60

Gly Leu Gln Thr Ser Gln Asp Ala Arg Phe Tyr Ala Leu Ser Ala Arg  
65 70 75 80

Phe Glu Pro Phe Ser Asn Lys Gly Gln Pro Leu Val Val Gln Pro Ala  
85 90 95

crt sequences.ST25

Arg Thr Pro Ala Ser Thr Pro Cys Arg Pro Asp Ser Ser Arg Ser Ala  
100 105 110

Thr Arg Ala Ser His Trp Trp Cys Ser Ser Pro  
115 120

<210> 14  
<211> 12  
<212> PRT  
<213> Artificial

<220>  
<223> Synthetic Construct

<400> 14

Asn Thr Ser Arg Thr Leu Thr Ala Gly Ala Ala Thr  
1 5 10

<210> 15  
<211> 45  
<212> PRT  
<213> Artificial

<220>  
<223> Synthetic Construct

<400> 15

Ser Cys Phe Arg Pro Ala Trp Thr Arg Arg Thr Cys Thr Gly Thr Leu  
1 5 10 15

Ser Thr Thr Ser Cys Leu Val Leu Thr Ser Val Ala Pro Ala Pro Arg  
20 25 30

Arg Phe Thr Ser Ser Ser Thr Thr Arg Ala Arg Thr Cys  
35 40 45

<210> 16  
<211> 17  
<212> PRT  
<213> Artificial

<220>  
<223> Synthetic Construct

<400> 16

Ser Thr Arg Thr Ser Val Ala Arg Thr Thr Ser Ser His Thr Cys Thr  
1 5 10 15

Arg

crt sequences.ST25

<210> 17  
<211> 9  
<212> PRT  
<213> Artificial

<220>  
<223> Synthetic Construct

<400> 17

Ser Cys Gly Arg Thr Thr Arg Met Arg  
1 5

<210> 18  
<211> 23  
<212> PRT  
<213> Artificial

<220>  
<223> Synthetic Construct

<400> 18

Arg Leu Thr Thr Ala Arg Trp Ser Arg Ala Pro Trp Arg Met Thr Gly  
1 5 10 15

Thr Ser Tyr Pro Pro Arg Arg  
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<210> 19  
<211> 56  
<212> PRT  
<213> Artificial

<220>  
<223> Synthetic Construct

<400> 19

Arg Thr Gln Met Pro Arg Ser Leu Lys Thr Gly Thr Ser Gly Pro Arg  
1 5 10 15

Ser Thr Thr Pro Arg Thr Pro Ser Pro Arg Thr Gly Thr Ser Pro Ser  
20 25 30

Thr Ser Pro Thr Arg Thr Arg Arg Ser Pro Lys Thr Gly Thr Lys Lys  
35 40 45

Trp Thr Glu Ser Gly Ser Arg Arg  
50 55

<210> 20  
<211> 91  
<212> PRT  
<213> Artificial

crt sequences.ST25

<220>

<223> Synthetic Construct

<400> 20

Phe Arg Thr Pro Ser Thr Arg Val Ser Gly Ser Arg Gly Arg Ser Thr  
1 5 10 15

Thr Pro Ile Thr Lys Ala Pro Gly Ser Thr Pro Lys Ser Thr Thr Pro  
20 25 30

Ser Thr Arg Pro Thr Leu Thr Ser Met Pro Thr Thr Ala Leu Pro Cys  
35 40 45

Trp Ala Trp Thr Ser Gly Arg Ser Ser Arg Ala Pro Ser Ser Thr Thr  
50 55 60

Ser Ser Ser Pro Thr Met Arg Arg Thr Gln Arg Ser Leu Ala Thr Arg  
65 70 75 80

Arg Gly Ala Ser Pro Arg Arg Pro Arg Ser Arg  
85 90

<210> 21

<211> 9

<212> PRT

<213> Artificial

<220>

<223> Synthetic Construct

<400> 21

Lys Thr Ser Arg Thr Arg Ser Ser Gly  
1 5

<210> 22

<211> 63

<212> PRT

<213> Artificial

<220>

<223> Synthetic Construct

<400> 22

Arg Arg Arg Arg Arg Arg Ser Gly Arg Arg Arg Arg Pro Arg  
1 5 10 15

Arg Thr Arg Arg Thr Arg Thr Arg Arg Thr Arg Met Arg Thr Arg  
20 25 30

Arg Thr Arg Thr Arg Arg Arg Arg Pro Pro Ala Ser Ser Thr  
Page 13

35

40

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45

His Met Met Phe Leu Thr Met Leu Asp Arg Pro Arg Thr Ser Cys  
50 55 60

<210> 23  
<211> 418  
<212> PRT  
<213> Artificial

<220>  
<223> CRT peptide sequence from CRT cDNA

<400> 23

Met Leu Leu Pro Val Pro Leu Leu Leu Gly Leu Leu Gly Leu Ala Ala  
1 5 10 15

Ala Glu Pro Val Val Tyr Phe Lys Glu Gln Phe Leu Asp Gly Asp Gly  
20 25 30

Trp Thr Glu Arg Trp Ile Glu Ser Lys His Lys Ser Asp Phe Gly Lys  
35 40 45

Phe Val Leu Ser Ser Gly Lys Phe Tyr Gly Asp Gln Glu Lys Asp Lys  
50 55 60

Gly Leu Gln Thr Ser Gln Asp Ala Arg Phe Tyr Ala Leu Ser Ala Arg  
65 70 75 80

Phe Glu Pro Phe Ser Asn Lys Gly Gln Pro Leu Val Val Gln Phe Thr  
85 90 95

Val Lys His Glu Gln Asn Ile Asp Cys Gly Gly Gly Tyr Val Lys Leu  
100 105 110

Phe Pro Ala Gly Leu Asp Gln Lys Asp Met His Gly Asp Ser Glu Tyr  
115 120 125

Asn Ile Met Phe Gly Pro Asp Ile Cys Gly Pro Gly Thr Lys Lys Val  
130 135 140

His Val Ile Phe Asn Tyr Lys Gly Lys Asn Val Leu Ile Asn Lys Asp  
145 150 155 160

Ile Arg Cys Lys Asp Asp Glu Phe Thr His Leu Tyr Thr Leu Ile Val  
165 170 175

Arg Pro Asp Asn Thr Tyr Glu Val Lys Ile Asp Asn Ser Gln Val Glu  
180 185 190

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Ser Gly Ser Leu Glu Asp Asp Trp Asp Phe Leu Pro Pro Lys Lys Ile  
195 200 205

Lys Asp Pro Asp Ala Ser Lys Pro Glu Asp Trp Asp Glu Arg Ala Lys  
210 215 220

Ile Asp Asp Pro Thr Asp Ser Lys Pro Glu Asp Trp Asp Lys Pro Glu  
225 230 235 240

His Ile Pro Asp Pro Asp Ala Lys Lys Pro Glu Asp Trp Asp Glu Glu  
245 250 255

Met Asp Gly Glu Trp Glu Pro Pro Val Ile Gln Asn Pro Glu Tyr Lys  
260 265 270

Gly Glu Trp Lys Pro Arg Gln Ile Asp Asn Pro Asp Tyr Lys Gly Thr  
275 280 285

Trp Ile His Pro Glu Ile Asp Asn Pro Glu Tyr Ser Pro Asp Ala Asn  
290 295 300

Ile Tyr Ala Tyr Asp Ser Phe Ala Val Leu Gly Leu Asp Leu Trp Gln  
305 310 315 320

Val Lys Ser Gly Thr Ile Phe Asp Asn Phe Leu Ile Thr Asn Asp Glu  
325 330 335

Ala Tyr Ala Glu Glu Phe Gly Asn Glu Thr Trp Gly Val Thr Lys Thr  
340 345 350

Ala Glu Lys Gln Met Lys Asp Lys Gln Asp Glu Glu Gln Arg Leu Lys  
355 360 365

Glu Glu Glu Glu Glu Lys Lys Arg Lys Glu Glu Glu Glu Ala Glu Glu  
370 375 380

Asp Glu Glu Asp Lys Asp Asp Lys Glu Asp Glu Asp Glu Asp Glu Glu  
385 390 395 400

Asp Lys Asp Glu Glu Glu Glu Ala Ala Ala Gly Gln Ala Lys Asp  
405 410 415

Glu Leu

crt sequences.ST25

<211> 430  
<212> PRT  
<213> Artificial

<220>  
<223> CRT peptide sequence with HA tag inserted into peptide

<220>  
<221> MISC\_FEATURE  
<222> (413)..(424)  
<223> HA Tag

<400> 24

Met Leu Leu Pro Val Pro Leu Leu Leu Gly Leu Leu Gly Leu Ala Ala  
1 5 10 15

Ala Glu Pro Val Val Tyr Phe Lys Glu Gln Phe Leu Asp Gly Asp Gly  
20 25 30

Trp Thr Glu Arg Trp Ile Glu Ser Lys His Lys Ser Asp Phe Gly Lys  
35 40 45

Phe Val Leu Ser Ser Gly Lys Phe Tyr Gly Asp Gln Glu Lys Asp Lys  
50 55 60

Gly Leu Gln Thr Ser Gln Asp Ala Arg Phe Tyr Ala Leu Ser Ala Arg  
65 70 75 80

Phe Glu Pro Phe Ser Asn Lys Gly Gln Pro Leu Val Val Gln Phe Thr  
85 90 95

Val Lys His Glu Gln Asn Ile Asp Cys Gly Gly Gly Tyr Val Lys Leu  
100 105 110

Phe Pro Ala Gly Leu Asp Gln Lys Asp Met His Gly Asp Ser Glu Tyr  
115 120 125

Asn Ile Met Phe Gly Pro Asp Ile Cys Gly Pro Gly Thr Lys Lys Val  
130 135 140

His Val Ile Phe Asn Tyr Lys Gly Lys Asn Val Leu Ile Asn Lys Asp  
145 150 155 160

Ile Arg Cys Lys Asp Asp Glu Phe Thr His Leu Tyr Thr Leu Ile Val  
165 170 175

Arg Pro Asp Asn Thr Tyr Glu Val Lys Ile Asp Asn Ser Gln Val Glu  
180 185 190

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Ser Gly Ser Leu Glu Asp Asp Trp Asp Phe Leu Pro Pro Lys Lys Ile  
195 200 205

Lys Asp Pro Asp Ala Ser Lys Pro Glu Asp Trp Asp Glu Arg Ala Lys  
210 215 220

Ile Asp Asp Pro Thr Asp Ser Lys Pro Glu Asp Trp Asp Lys Pro Glu  
225 230 235 240

His Ile Pro Asp Pro Asp Ala Lys Lys Pro Glu Asp Trp Asp Glu Glu  
245 250 255

Met Asp Gly Glu Trp Glu Pro Pro Val Ile Gln Asn Pro Glu Tyr Lys  
260 265 270

Gly Glu Trp Lys Pro Arg Gln Ile Asp Asn Pro Asp Tyr Lys Gly Thr  
275 280 285

Trp Ile His Pro Glu Ile Asp Asn Pro Glu Tyr Ser Pro Asp Ala Asn  
290 295 300

Ile Tyr Ala Tyr Asp Ser Phe Ala Val Leu Gly Leu Asp Leu Trp Gln  
305 310 315 320

Val Lys Ser Gly Thr Ile Phe Asp Asn Phe Leu Ile Thr Asn Asp Glu  
325 330 335

Ala Tyr Ala Glu Glu Phe Gly Asn Glu Thr Trp Gly Val Thr Lys Thr  
340 345 350

Ala Glu Lys Gln Met Lys Asp Lys Gln Asp Glu Glu Gln Arg Leu Lys  
355 360 365

Glu Glu Glu Glu Glu Lys Lys Arg Lys Glu Glu Glu Glu Ala Glu Glu  
370 375 380

Asp Glu Glu Asp Lys Asp Asp Lys Glu Asp Glu Asp Glu Asp Glu Glu  
385 390 395 400

Asp Lys Asp Glu Glu Glu Glu Ala Ala Ala Gly Leu Glu Tyr Pro  
405 410 415

Tyr Asp Val Pro Asp Tyr Ala Arg Gln Ala Lys Asp Glu Leu  
420 425 430